-1-SEQUENCE LISTING

<110> Lee, Richard T. Landschulz, Katherine T. Turi, Thomas G. Thompson, John F. Kennedy, Scott P.

Applicants: Richard T. Lee, et al. Serial No: Unassigned Filed: Herewith, August 21, 2001 Title: DIAGNOSIS AND TREATMENT OF CARDIOVASCULAR CONDITIONS Express Mail No: EL844533521US

> 60 120

<120> DIAGNOSIS AND TREATMENT OF CARDIOVASCULAR CONDITIONS

<130> P0738/7001/ERP/KA

<150> US 60/227,159 <151> 2000-08-22

<160> 17

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1321

<212> DNA

<213> Homo Sapiens

<220>

<221> CDS

<222> (413)...(1273)

<400> 1

ggcggcagcg cgcgcc acgcccccgg ggctgc tgagccccgc ggcgcc ctcccccgcc gcgcgc	cegag gggaggeegg gg ceegg gaaettggeg ge cetee tgeatgeggg ge	ttccggac gccacccgcg (gggcgcag cggagcgcgg (gacccgag cccggcgagc (cccagctc cgggcgccgg (gccgcgcc gccgccgt (tecegegeae 240 eggggegege 300 eeggageeee 360
2 2 2 2 2 2 2 2		gcc gcc gcc gcc ggg Ala Ala Ala Ala Gly 15	2
	2 2 2	cgc tct ttg ttc cag Arg Ser Leu Phe Gln 30	
		atc atc atc atc gtg Ile Ile Ile Ile Val 45	
Met Met Val Met V		tgc ctg ctg agc cac Cys Leu Leu Ser His 60	
2 2		cac agc cag ggg cgg His Ser Gln Gly Arg 80	
	2 22 2	ctg tgg ccc tcg gag Leu Trp Pro Ser Glu	_

cgaccgcggt ctcggagcga aacccgatct ccttggactt gaatgaggag gaggaggcgg

cggcggcggc ggcggcggag gcgctcggct ggggaaagct agcggcagag gctcagcccc

		85					90					95				
								_	_	-		_	_	cct Pro		754
		_	_	_	_		_			_	_			cgc Arg		802
	_		-				-		_	_				gac Asp 145	_	850
														tac Tyr		898
		-			_			_			_	-	_	gaa Glu	-	946
														gac Asp		994
														agc Ser		1042
	_			-	-	_	_			_			_	atg Met 225		1090
														GJÀ āāā		1138
														gag Glu		1186
														gcc Ala		1234
								aaa Lys					tago	ggtco	ccc	1283
aggo	gggg	ccg g	ggct	gggg	ct go	cgtaç	ggtga	a aaa	aggca	ag					•	1321
		210>														
		/	201													

<211> 287 <212> PRT

<213> Homo Sapiens

<400> 2

Met His Arg Leu Met Gly Val Asn Ser Thr Ala Ala Ala Ala Gly 5 10 1 Gln Pro Asn Val Ser Cys Thr Cys Asn Cys Lys Arg Ser Leu Phe Gln

```
25
            20
Ser Met Glu Ile Thr Glu Leu Glu Phe Val Gln Ile Ile Ile Val
Val Val Met Met Val Met Val Val Ile Thr Cys Leu Leu Ser His
Tyr Lys Leu Ser Ala Arg Ser Phe Ile Ser Arg His Ser Gln Gly Arg
                    70
Arg Arg Glu Asp Ala Leu Ser Ser Glu Gly Cys Leu Trp Pro Ser Glu
                                    90
Ser Thr Val Ser Gly Asn Gly Ile Pro Glu Pro Gln Val Tyr Ala Pro
                                105
Pro Arg Pro Thr Asp Arg Leu Ala Val Pro Pro Phe Ala Gln Arg Glu
        115
                            120
Arg Phe His Arg Phe Gln Pro Thr Tyr Pro Tyr Leu Gln His Glu Ile
                        135
Asp Leu Pro Pro Thr Ile Ser Leu Ser Asp Gly Glu Glu Pro Pro
                    150
                                        155
Tyr Gln Gly Pro Cys Thr Leu Gln Leu Arg Asp Pro Glu Gln Gln Leu
                165
                                    170
Glu Leu Asn Arg Glu Ser Val Arg Ala Pro Pro Asn Arg Thr Ile Phe
            180
                                185
Asp Ser Asp Leu Met Asp Ser Ala Arg Leu Gly Gly Pro Cys Pro Pro
        195
Ser Ser Asn Ser Gly Ile Ser Ala Thr Cys Tyr Gly Ser Gly Gly Arg
                        215
                                            220
Met Glu Gly Pro Pro Pro Thr Tyr Ser Glu Val Ile Gly His Tyr Pro
                    230
Gly Ser Ser Phe Gln His Gln Gln Ser Ser Gly Pro Pro Ser Leu Leu
                                    250
                245
Glu Gly Thr Arg Leu His His Thr His Ile Ala Pro Leu Glu Ser Ala
                                265
Ala Ile Trp Ser Lys Glu Lys Asp Lys Gln Lys Gly His Pro Leu
        275
                            280
      <210> 3
      <211> 861
      <212> DNA
      <213> Homo Sapiens
      <220>
      <221> CDS
      <222> (1)...(861)
      <400> 3
atgcaccgct tgatggggt caacagcacc gccgccgccg ccgccgggca gcccaatgtc
                                                                        60
tectgeaegt geaactgeaa aegetetttg ttecagagea tggagateae ggagetggag
                                                                       120
tttgttcaga tcatcatcat cgtggtggtg atgatggtga tggtggtggt gatcacgtgc
                                                                       180
ctgctgagcc actacaagct gtctgcacgg tccttcatca gccggcacag ccaggggcgg
                                                                       240
                                                                       300
aggagagaag atgccctgtc ctcagaagga tgcctgtggc cctcggagag cacagtgtca
ggcaacggaa teccagagee geaggtetae geeeegeete ggeeeacega eegeetggee
                                                                       360
gtgccgccct tcgcccagcg ggagcgcttc caccgcttcc agcccaccta tccgtacctg
                                                                       420
cagcacgaga tcgacctgcc acccaccatc tcgctgtcag acggggagga gcccccaccc
                                                                       480
                                                                       540
taccagggcc cctgcaccct ccagcttcgg gaccccgagc agcagctgga actgaaccgg
gagtcggtgc gcgcaccccc aaacagaacc atcttcgaca gtgacctgat ggatagtgcc
                                                                       600
aggetgggeg geeectgeec eeceageagt aactegggea teagegeeac gtgetaegge
                                                                       660
                                                                       720
ageggeggge geatggaggg geegeegeee acetacageg aggteategg ceactaceeg
gggtcctcct tccagcacca gcagagcagt gggccgccct ccttgctgga ggggacccgg
                                                                       780
                                                                       840
ctccaccaca cacacatcgc gcccctagag agcgcagcca tctggagcaa agagaaggat
                                                                       861
aaacagaaag gacaccctct c
```

	<2	211> 212> 213>		o Sap	piens	5											
	<2 <2	222>	CDS (7)	(4	474)												
ctca	acc a	_	cgt d			cgc a Arg s	-	_		_		_			_		48
_	gcc Ala	_		_	_					_							96
	ggt Gly							_			_			_		·	144
_	cct Pro	_		-		-	-		_			_		_	-	;	192
	agg Arg															:	240
	ccg Pro 80																288
	tgc Cys	_		_	_	_	-				_			_			336
	gag Glu	_	-			-	-		_							:	384
	gtc Val																432
	gac Asp																474
taa																	477
	<2 <2	210> 211> 212> 213>	156	o Sag	piens	5											
Mot	<4 Cys	400>		7) ** ~	Ser	Cve	шie	Dro	Th≻	Me+	Thγ	Tle	Lev	Gla	Δl =		
1	Thr			5					10					15			

								-5-							
Glu		20 Phe	Thr	Phe	Asp		25 Leu	Pro	Glu	Pro		30 Ala	Ala	Pro	
		Pro	Ser	Ala			Gly	His	Arg			Ser	Arg	Arg	
	Tyr	Pro	Arg	Val 70		Arg	Arg	Gln	Leu 75		Val	Glu	Glu	Pro 80	
Pro	Ala	Lys	Arg 85	Leu	Leu	Phe	Leu	Leu 90	Leu	Thr	Ile	Val	Phe 95	Cys	
ılle	Leu	Met 100	Ala	Glu	Glu	Gly	Val 105	Pro	Ala	Pro	Leu	Pro 110	Pro	Glu	
Ala	Pro 115	Asn	Ala	Ala	Ser	Leu 120	Ala	Pro	Thr	Pro	Val 125	Ser	Pro	Val	
Glu 130	Pro	Phe	Asn	Leu	Thr 135	Ser	Glu	Pro	Ser	Asp 140	Tyr	Ala	Leu	Asp	
	Thr	Phe	Leu	Gln 150	Gln	His	Pro	Ala	Ala 155	Phe			•		
<2 <2 <2	211> 212> 213> 220>	2704 DNA Homo		piens	5										
<2	222>	(222		.(139	94)										
tagto catto taaao	gta a tgt t	accaq ttaaa	atcti	a tt	ttat	tttt	aaq	gctca				gaa 1	tacct		60 120
ccgt										c at	et Va	g at	tg tt	ettett ee aag ne Lys 5	180 236
accgto g atc s Ile	cat t aag	tct tct	aact ttt	ct ta gag	aaaa gtg	ccaa gtc	ttt	agtto aac	gac	c at	et Va L gaa	al Me	tg tt et Pl gtg	tac aag ne Lys 5	
, atc	aag Lys ggc	tct tct Ser gag	ttt Phe 10	gag Glu gtg	gtg Val gct	gtc Val ggc	ttt Phe cgg	agtto aac Asn 15 gtg	gac Asp ata	c at Me	g gtet Valuet Va	al Me aag Lys gtg	tg ttet Ph gtg Val 20	tac aag tac Tyr	236
g atc s Ile	aag Lys ggc Gly	tct Ser gag Glu 25	ttt Phe 10 agg Arg	gag Glu gtg Val	gtg Val gct Ala	gtc Val ggc Gly	ttt Phe cgg Arg 30	aac Asn 15 gtg Val	gac Asp ata Ile	c at Me	gggt Valuet Valu	aag Lys gtg Val 35	gtg gtg Val 20 tgt Cys	tac Tyr gaa Glu	284
g atc s Ile c agt v Ser	aag Lys ggc Gly cgt Arg 40	tct Ser gag Glu 25 gtc Val	ttt Phe 10 agg Arg aaa Lys	gag Glu gtg Val gcc Ala	gtg Val gct Ala gtt Val	gtc Val ggc Gly agg Arg 45	ttt Phe cgg Arg 30 atc Ile	aac Asn 15 gtg Val ctg Leu	gac Asp ata Ile gct Ala	c at Me	gaa Glu gga Gly 50 act	aag Lys gtg Val 35 gtg Val tcg	gtg Val 20 tgt Cys gct Ala	tac aag tac Tyr gaa Glu aaa Lys	284
g atc s Ile c agt s Ser c act Thr	aag Lys ggc Gly cgt Arg 40 tgg Trp	tct Ser gag Glu 25 gtc Val atg Met	ttt Phe 10 agg Arg aaa Lys cag Gln	gag Glu gtg Val gcc Ala gga Gly	gtg Val gct Ala gtt Val tcc Ser 60	gtc Val ggc Gly agg Arg 45 cag	ttt Phe cgg Arg 30 atc Ile cag Gln	aac Asn 15 gtg Val ctg Leu tgc Cys	gac Asp ata Ile gct Ala aaa Lys	c at Me I cct Pro gtg Val tgc Cys cag Gln 65 cag	gaa Glu gag Glu gga Gly 50 act Thr	aag Lys gtg Val 35 gtg Val tcg Ser aca	gtg Val 20 tgt Cys gct Ala gag Glu	tac aag ne Lys 5 tac Tyr gaa Glu aaa Lys tac Tyr	236 284 332 380
g atc s Ile s agt s Ser act Thr ctt Leu 55 s cgc	aag Lys ggc Gly cgt Arg 40 tgg Trp tat Tyr	tct Ser gag Glu 25 gtc Val atg Met gaa Glu	ttt Phe 10 agg Arg aaa Lys cag Gln gac Asp	gag Glu gtg Val gcc Ala gga Gly acg Thr 75	gtg Val gct Ala gtt Val tcc Ser 60 ctt Leu aga	gtc Val ggc Gly agg Arg 45 cag Gln ctt Leu	ttt Phe cgg Arg 30 atc Ile cag Gln ctg Leu	aac Asn 15 gtg Val ctg Leu tgc Cys	gac Asp ata Ile gct Ala aaa Lys gac Asp 80	c at Me 1 cct Pro gtg Val tgc Cys cag Gln 65 cag Gln tat	gaa Glu gag Glu ggay 50 act Thr	aag Lys gtg Val 35 gtg Val tcg Ser aca Thr	gtg Val 20 tgt Cys gct Ala gag Glu ggt Gly aag	tac aag ne Lys 5 tac Tyr gaa Glu aaa Lys tac Tyr gag Glu 85	236 284 332 380
	a Gly 50 Leu 1 Pro 1 Ile 2 Ala 1 Glu 130 Ser 5 Citagto	35 a Gly Arg 50 Leu Tyr a Pro Ala a Ile Leu b Ala Pro 115 a Glu Pro 130 a Ser Thr c <210> <211> <221> <221> <221> <222> <223> <400> ctagtgta a acatttgt a	35 a Gly Arg Pro 50 b Leu Tyr Pro a Pro Ala Lys a Ile Leu Met 100 b Ala Pro Asn 115 a Glu Pro Phe 130 b Ser Thr Phe 5 c <210> 6 <211> 270 <212> DNA <213> Homo <220> <221> CDS <222> (223 <203> VDU <400> 6 ctagtgta accae ccatttgt ttaac ccatttgt ttaac	35 a Gly Arg Pro Ser 50 Leu Tyr Pro Arg b Pro Ala Lys Arg 85 a Ile Leu Met Ala 100 b Ala Pro Asn Ala 115 a Glu Pro Phe Asn 130 a Ser Thr Phe Leu 5 c 210> 6 c 211> 2704 c 212> DNA c 213> Homo Sag c 220> c 221> CDS c 222> (222) c 223> VDUP1 c 400> 6 c tagtgta accagcggo	35 a Gly Arg Pro Ser Ala 50 Leu Tyr Pro Arg Val 70 a Pro Ala Lys Arg Leu 85 a Ile Leu Met Ala Glu 100 b Ala Pro Asn Ala Ala 115 a Glu Pro Phe Asn Leu 130 a Ser Thr Phe Leu Gln 5 5 5 5 6 6 7 7 7 7 7 8 7 8 7 8 8 7 8 8 8 8 8 8	35 a Gly Arg Pro Ser Ala Ser 50 55 Leu Tyr Pro Arg Val Val 70 a Pro Ala Lys Arg Leu Leu 85 a Ile Leu Met Ala Glu Glu 100 b Ala Pro Asn Ala Ala Ser 115 a Glu Pro Phe Asn Leu Thr 130 135 a Ser Thr Phe Leu Gln Gln 5 c 210> 6 c 211> 2704 c 212> DNA c 213> Homo Sapiens <220> c 221> CDS c 222> (222)(1394) c 223> VDUP1 c 400> 6 ctagtgta accagcggcg tatatt	35 40 A Gly Arg Pro Ser Ala Ser Arg 50 55 Leu Tyr Pro Arg Val Val Arg 70 A Pro Ala Lys Arg Leu Leu Phe 85 A Ile Leu Met Ala Glu Glu Gly 100 Ala Pro Asn Ala Ala Ser Leu 115 120 A Glu Pro Phe Asn Leu Thr Ser 130 135 A Ser Thr Phe Leu Gln Gln His 50 <210> 6 <211> 2704 <212> DNA <213> Homo Sapiens <220> <221> CDS <222> (222)(1394) <223> VDUP1 <400> 6 ctagtgta accagcggcg tatattttte ccatttgt ttaaatctta tttatttte ccatttgt ttaaatctta tttatttte	35	35	35	35	35	35	35	A Gly Arg Pro Ser Ala Ser Arg Gly His Arg Lys Arg Ser Arg Arg 50

-6-

Gly	Phe	Glu	Leu 105	Pro	Gln	Gly	Pro	Leu 110	Gly	Thr	Ser	Phe	Lys 115	Gly	Lys	
		tgt Cys 120														620
_		act Thr				_				-	-		_	_		668
		aat Asn														716
_		gtt Val		-	_				-					-		764
		att Ile														812
	_	gac Asp 200					_		_			_			-	860
		gtg Val														908
		cag Gln														956
		gca Ala														1004
		atc Ile	_		_				_	_	_				_	1052
		gtt Val 280														1100
		att Ile														1148
		cga Arg														1196
		cca Pro														1244
		ttg Leu														1292

tct caa gac agc cct atc ttt atg tat gcc cct gag ttc aag ttc atg Ser Gln Asp Ser Pro Ile Phe Met Tyr Ala Pro Glu Phe Lys Phe Met 360 365 370	1340
cca cca ccg act tat act gag gtg gat ccc tgc atc ctc aac aac aat Pro Pro Pro Thr Tyr Thr Glu Val Asp Pro Cys Ile Leu Asn Asn Asn 375 380 385	1388
gtg cag tgagcatgtg gaagaaaaga agcagcttta cctacttgtt tctttttgtc Val Gln 390	1444
totottootg gacactoact ttttcagaga ctcaacagto togtcaatgg agtgtgggto	1504
caccttagcc tctgacttcc taatgtagga ggtggtcagc aggcaatctc ctgggcctta	1564
aaggatgcgg actcatcctc agccagcgcc catgttgtga tacaggggtg tttgttggat	1624
gggtttaaaa ataactagaa aaactcaggc ccatccattt tctcagatct ccttgaaaat	1684
tgaggccttt tcgatagttt cgggtcaggt aaaaatggcc tcctggcgta agcttttcaa	1744
ggttttttgg aggctttttg taaattgtga taggaacttt ggaccttgaa cttacgtatc	1804
atgtggagaa gagccaattt aacaaactag gaagatgaaa agggaaattg tggccaaaac	1864
tttgggaaaa ggaggttett aaaateagtg ttteeeettt gtgeaettgt agaaaaaaa	1924
gaaaaacctt ctagagctga tttgatggac aatggagaga gctttccctg tgattataaa	1984
aaaggaaget agetgeteta eggteatett tgettagagt ataetttaae etggetttta	2044
aagcagtagt aactgcccca ccaaaggtct taaaagccat ttttggagcc tattgcactg	2104
tgttctccta ctgcaaatat tttcatatgg gaggatggtt ttctcttcat gtaagtcctt	2164
ggaattgatt ctaaggtgat gttcttagca ctttaattcc tgtcaaattt tttgttctcc	2224
ccttctgcca tcttaaatgt aagctgaaac tggtctactg tgtctctagg gttaagccaa	2284
aagacaaaaa aaattttact acttttgaga ttgccccaat gtacagaatt atataattct	2344
aacgettaaa teatgtgaaa gggttgetge tgteageett geeeactgtg actteaaace	2404
caaggaggaa ctcttgatca agatgcccaa ccctgtgatc agaacctcca aatactgcca	2464
tgagaaacta gagggcaggt gttcataaaa gccctttgaa cccccttcct gccctgtgtt	2524
aggagatagg gatattggcc cctcactgca gctgccagca cttggtcagt cactctcagc	2584
catagcactt tgttcactgt cctgtgtcag agcactgagc tccacccttt tctgagagtt	2644
attacagcca gaaagtgtgg gctgaagatg gttggtttca tgtgggggta ttatgtaccc	2704
<210> 7 <211> 391 <212> PRT <213> Homo Sapiens	

<400> 7

Met Val Met Phe Lys Lys Ile Lys Ser Phe Glu Val Val Phe Asn Asp 5 Pro Glu Lys Val Tyr Gly Ser Gly Glu Arg Val Ala Gly Arg Val Ile 25 30 Val Glu Val Cys Glu Val Thr Arg Val Lys Ala Val Arg Ile Leu Ala 40 Cys Gly Val Ala Lys Val Leu Trp Met Gln Gly Ser Gln Gln Cys Lys Gln Thr Ser Glu Tyr Leu Arg Tyr Glu Asp Thr Leu Leu Glu Asp 75 . 80 70 Gln Pro Thr Gly Glu Asn Glu Met Val Ile Met Arg Pro Gly Asn Lys 90 Tyr Glu Tyr Lys Phe Gly Phe Glu Leu Pro Gln Gly Pro Leu Gly Thr 105 Ser Phe Lys Gly Lys Tyr Gly Cys Val Asp Tyr Trp Val Lys Ala Phe 120 Leu Asp Arg Pro Ser Gln Pro Thr Gln Glu Thr Lys Lys Asn Phe Glu 130 135 Val Val Asp Leu Val Asp Val Asn Thr Pro Asp Leu Met Ala Pro Val

```
150
                                         155
Ser Ala Lys Lys Glu Lys Lys Val Ser Cys Met Phe Ile Pro Asp Gly
                                    170
Arg Val Ser Val Ser Ala Arg Ile Asp Arg Lys Gly Phe Cys Glu Gly
                                185
                                                     190
Asp Glu Ile Ser Ile His Ala Asp Phe Glu Asn Thr Cys Ser Arg Ile
                            200
Val Val Pro Lys Ala Ala Ile Val Ala Arg His Thr Tyr Leu Ala Asn
                        215
                                             220
Gly Gln Thr Lys Val Leu Thr Gln Lys Leu Ser Ser Val Arg Gly Asn
                    230
                                         235
His Ile Ile Ser Gly Thr Cys Ala Ser Trp Arg Gly Lys Ser Leu Arg
                                    250
                245
Val Gln Lys Ile Arg Pro Ser Ile Leu Gly Cys Asn Ile Leu Arg Val
                                265
Glu Tyr Ser Leu Leu Ile Tyr Val Ser Val Pro Gly Ser Lys Lys Val
                            280
Ile Leu Asp Leu Pro Leu Val Ile Gly Ser Arg Ser Gly Leu Ser Ser
                        295
                                             300
Arg Thr Ser Ser Met Ala Ser Arg Thr Ser Ser Glu Met Ser Trp Val
                    310
                                         315
Asp Leu Asn Ile Pro Asp Thr Pro Glu Ala Pro Pro Cys Tyr Met Asp
                                     330
Val Ile Pro Glu Asp His Arg Leu Glu Ser Pro Thr Thr Pro Leu Leu
                                345
Asp Asp Met Asp Gly Ser Gln Asp Ser Pro Ile Phe Met Tyr Ala Pro
                            360
Glu Phe Lys Phe Met Pro Pro Pro Thr Tyr Thr Glu Val Asp Pro Cys
                        375
Ile Leu Asn Asn Asn Val Gln
385
                    390
      <210> 8
      <211> 2717
      <212> DNA
      <213> Homo Sapiens
      <220>
      <221> CDS
      <222> (72)...(545)
      <223> BTG2
      <400> 8
cagggtaacg ctgtcttgtg gacccgcact tcccacccga gacctctcac tgagcccgag
                                                                       60
ccgcgcgcga c atg agc cac ggg aag gga acc gac atg ctc ccg gag atc
                                                                      110
             Met Ser His Gly Lys Gly Thr Asp Met Leu Pro Glu Ile
gee gee geg gtg gge tte etc tee age etc etg agg ace egg gge tge
                                                                      158
Ala Ala Ala Val Gly Phe Leu Ser Ser Leu Leu Arg Thr Arg Gly Cys
                         20
                                              25
                                                                      206
qtq aqc qaq cag agg ctt aag gtc ttc agc ggg gcg ctc cag gag gca
Val Ser Glu Gln Arg Leu Lys Val Phe Ser Gly Ala Leu Gln Glu Ala
                     35
                                          40
ctc aca gag cac tac aaa cac cac tgg ttt ccc gaa aag ccg tcc aag
                                                                      254
Leu Thr Glu His Tyr Lys His His Trp Phe Pro Glu Lys Pro Ser Lys
                                      55
qqc tcc ggc tac cgc tgc att cgc atc aac cac aag atg gac ccc atc
                                                                      302
```



-9-

Gly Ser Gly Tyr Arg (Cys Ile Arg	Ile Asn His	Lys Met Asp 75	Pro Ile
atc agc agg gtg gcc a Ile Ser Arg Val Ala 9 80				
cag ctg ctg ccc agc (Gln Leu Leu Pro Ser (95				
tcc tac cgc att ggg (Ser Tyr Arg Ile Gly (110				
gcc cca ctg gcc gcc t Ala Pro Leu Ala Ala S 130				
ctg ctg ggc cgg agc a Leu Leu Gly Arg Ser S 145				
age taggeeette egeee				
caacaggcca ccacatacct				
atatattatt tttttttaag aatccttcaa gggagctgct				
cgtgcttgag tctgtgagc				
ctagccaagg agaagtggg				,,,,,
agcaaggtta gcaactgtga				
caagttcaga gctctctgto				
tcaggggcat tcatgcctg		-		
atgaggtcct gggcagagag ttcttgaaat catgacttg				
agccaggaat ctaaagctt				
gggttaggat ggaagggaad				, , ,
tatgtgtggc aaataatttg				
cactggggat gttttttgg				
tgctgccatg atccctttg		_		
tactgccttc ttttcaaaaq gtcgggtcat agagctaccq				
cccctqqqt cccaggagg				<i></i>
gtgggcttag ggaaccatc			_	
gcatgtattc cttggctgaa				
ttgtagggcc gacactaaat				
cagagcacct gtgggaaagg tgtgcaatat atactgttg				
ccttccttca atttctcagi				,
aaccgaatca ccttaagaag				, ,
ctgttgcccc ttagtgagga	atcttcacco	cacttcctct	acccccaggt	tctcctcccc 2155
acagecagte ceettteete				
accaaacact ctccctacco				
tgtattgcct tcccagacct				
ctgtgttctt gcatcttgto	tqcaaacagg	tccctacctt	tttagaagca	gcctcatggt 2455
ctcatgctta atcttgtcto	tcttctcttc	tttatgatgt	tcactttaaa	aacaacaaaa 2515
cccctgagct ggactgttg	gcaggcctgt	ctctcctatt	aagtaaaaat	aaatagtagt 2575
agtatgtttg taagctatto				
tttatatgga agaatgtaca aatgtagtag gataaaaaa		aaatgtacac	CLLLLEGETA	ctttaataaa 2695 2717

	<2 <2	210> 211> 212> 213>	157 PRT	o Sar	oiens	5										
_	<4 Ser	100> His		Lys	Gly	Thr	Asp	Met	Leu 10	Pro	Glu	Ile	Ala	Ala 15	Ala	
l Val	Gly	Phe	Leu 20	Ser	Ser	Leu	Leu	Arg 25		Arg	Gly	Cys	Val 30		Glu	
Gln	Arg	Leu 35	Lys	Val	Phe	Ser	Gly 40	Ala	Leu	Gln	Glu	Ala 45	Leu	Thr	Glu	
His	Tyr 50	Lys	His	His	Trp	Phe 55	Pro	Glu	Lys	Pro	Ser 60	Lys	Gly	Ser	Gly	
Tyr 65	Arg	Cys	Ile	Arg	Ile 70	Asn	His	Lys	Met	Asp 75	Pro	Ile	Ile	Ser	Arg 80	
Val	Ala	Ser	Gln	Ile 85	Gly	Leu	Ser	Gln	Pro 90	Gln	Leu	His	Gln	Leu 95	Leu	
	Ser		100			_		105					110			
Ile	Gly	Glu 115	Asp	Gly	Ser	Ile	Cys 120	Val	Leu	Tyr	Glu	Glu 125	Ala	Pro	Leu	
Ala	Ala 130	Ser	Cys	Gly	Leu	Leu 135	Thr	Cys	Lys	Asn	Gln 140	Val	Leu	Leu	Gly	
Arg 145	Ser	Ser	Pro	Ser	Lys 150	Asn	Tyr	Val	Met	Ala 155	Val	Ser				
	<2 <2	210> 211> 212> 212>	1746 DNA		oiens	5										
	<2 <2	220> 221> 222> 223>	(60)		(1037	7)										
~~~		100>		agat (		at at	- 0 0 0 0			agat	asta	7000	220	2011	20200	59
atg	gat Asp	ctg	act	gcc	atc	tac	gag	agc	ctc	ctg	tcg	ctg	agc	cct		107
	ccc Pro															155
	tcc Ser															203
	gtc Val 50															251
	agc Ser															299
	cgc Arg	_														347

-11-85 90 95

				tcg Ser												395
				tgc Cys											4	443
				cgc Arg											4	491
				ttc Phe 150											į	539
				cac His											į	587
				cgc Arg	_	-		-				_			•	635
 _				cca Pro					-	-				_	•	683
	_			tcg Ser			_								7	731
				tct Ser 230											7	779
				acc Thr											8	327
		_	_	tgg Trp			_			_	_				8	375
				gga Gly											Ċ	923
				tct Ser											Ġ	971
				gtg Val 310											10	019
	tct Ser			gag Glu	tgad	caaaq	gtg a	actgo	ccg	gt ca	agat	cagct	=		10	067

ggatctcagc ggggagccac gtctcttgca ctgtggtctc tgcatggacc ccagggctgt 1127 qqqqacttqq qqqacaqtaa tcaaqtaatc cccttttcca qaatqcatta acccactccc 1187 ctgacctcac gctggggcag gtccccaagt gtgcaagctc agtattcatg atggtggggg 1247 atggagtgtc ttccgaggtt cttgggggaa aaaaaattgt agcatattta agggaggcaa 1307 tgaaccetct ccccacctc ttccctgccc aaatctgtct cctagaatct tatgtgctgt 1367 gaataatagg cottcactgc coctccagtt tttatagacc tgaggttcca gtgtctcctg 1427 gtaactggaa cctctcctga gggggaatcc tggtgctcaa attaccctcc aaaagcaagt 1487 agccaaagcc gttgccaaac cccacccata aatcaatggg ccctttattt atgacgactt 1547 tatttattct aatatgattt tatagtattt atatatattg ggtcgtctgc ttcccttgta 1607 tttttcttcc tttttttgta atattgaaaa cgacgatata attattataa gtagactata 1667 atatatttag taatatatat tattacctta aaagtctatt tttgtgtttt gggcattttt 1727 1746 aaataaacaa tctqaqtqt

<210> 11

<211> 326

<212> PRT

<213> Homo Sapiens

<400> 11

Met Asp Leu Thr Ala Ile Tyr Glu Ser Leu Leu Ser Leu Ser Pro Asp 10 1 Val Pro Val Pro Ser Asp His Gly Gly Thr Glu Ser Ser Pro Gly Trp 25 Gly Ser Ser Gly Pro Trp Ser Leu Ser Pro Ser Asp Ser Ser Pro Ser 40 45 Gly Val Thr Ser Arg Leu Pro Gly Arg Ser Thr Ser Leu Val Glu Gly Arg Ser Cys Gly Trp Val Pro Pro Pro Gly Phe Ala Pro Leu Ala 75 Pro Arg Leu Gly Pro Glu Leu Ser Pro Ser Pro Thr Ser Pro Thr Ala 8.5 90 Thr Ser Thr Thr Pro Ser Arg Tyr Lys Thr Glu Leu Cys Arg Thr Phe 105 110 Ser Glu Ser Gly Arg Cys Arg Tyr Gly Ala Lys Cys Gln Phe Ala His 120 125 Gly Leu Gly Glu Leu Arg Gln Ala Asn Arg His Pro Lys Tyr Lys Thr Glu Leu Cys His Lys Phe Tyr Leu Gln Gly Arg Cys Pro Tyr Gly Ser 160 Arg Cys His Phe Ile His Asn Pro Ser Glu Asp Leu Ala Ala Pro Gly 165 170 His Pro Pro Val Leu Arg Gln Ser Ile Ser Phe Ser Gly Leu Pro Ser 190 185 Gly Arg Arg Thr Ser Pro Pro Pro Gly Leu Ala Gly Pro Ser Leu 195 200 Ser Ser Ser Ser Phe Ser Pro Ser Ser Pro Pro Pro Pro Gly Asp 215 Leu Pro Leu Ser Pro Ser Ala Phe Ser Ala Ala Pro Gly Thr Pro Leu 230 240 Ala Arg Arg Asp Pro Thr Pro Val Cys Cys Pro Ser Cys Arg Arg Ala 245 250 Thr Pro Ile Ser Val Trp Gly Pro Leu Gly Gly Leu Val Arg Thr Pro 265 Ser Val Gln Ser Leu Gly Ser Asp Pro Asp Glu Tyr Ala Ser Ser Gly 275 280 Ser Ser Leu Gly Gly Ser Asp Ser Pro Val Phe Glu Ala Gly Val Phe 295 300 Ala Pro Pro Gln Pro Val Ala Ala Pro Arg Arg Leu Pro Ile Phe Asn 315 Arg Ile Ser Val Ser Glu



325

<210> 12 <211> 878 <212> DNA <213> Mus Musculus <220>

<222> (20)...(841)

<221> CDS

(20) (011)	
<pre>&lt;400&gt; 12 aattcgtcga catggcttg atg ggg gtc aac ggc acc gcc</pre>	
ggg cag ccc aat gtc tcc tgc gcg tgc aac tgc cag cgc t Gly Gln Pro Asn Val Ser Cys Ala Cys Asn Cys Gln Arg S 15 20	
ccc agc atg gag atc acg gag ctg gag ttc gtg caa atc g Pro Ser Met Glu Ile Thr Glu Leu Glu Phe Val Gln Ile v 30 35 40	
gtg gta gtg atg atg gtg atg gtt atg att acg tgc of Val Val Val Met Met Val Met Val Met Ile Thr Cys 1 45 50 55	
cac tac aag ctg tca gcc cgc tcc ttc atc agc cga cac a His Tyr Lys Leu Ser Ala Arg Ser Phe Ile Ser Arg His s 60 65 70	
agg agg aga gac gat gga ctg tcc tcg gaa gga tgc ctc t Arg Arg Arg Asp Asp Gly Leu Ser Ser Glu Gly Cys Leu 5 80 85	
gag agt acg gtg tca ggt gga atg ccg gag cca cag gtc f Glu Ser Thr Val Ser Gly Gly Met Pro Glu Pro Gln Val 1 95	
cct cgg ccc act gac cga ctc gct gtg ccc ccc ttc atc c Pro Arg Pro Thr Asp Arg Leu Ala Val Pro Pro Phe Ile ( 110 115 120	
cga ttc caa ccc acc tac ccc tac ctg cag cac gaa att c Arg Phe Gln Pro Thr Tyr Pro Tyr Leu Gln His Glu Ile i 125 130 135	
ccc acc atc tca ctg tct gat ggg gag gag ccc cca ccc f Pro Thr Ile Ser Leu Ser Asp Gly Glu Glu Pro Pro Pro 140 145 150	
ccc tgc acc ctc cag cta cgg gac cct gag caa cag ctg c Pro Cys Thr Leu Gln Leu Arg Asp Pro Glu Gln Gln Leu G 160 165	
cgg gaa tot gtg cgc gca ccc cct aac cgg acc atc ttc c Arg Glu Ser Val Arg Ala Pro Pro Asn Arg Thr Ile Phe A	
ctt ata gac agc acc atg ctg ggg ggc ccc tgt ccc ccc a	agc agt aac 628



## -14-

_								-	14-								
Leu	Ile	Asp 190	Ser	Thr	Met	Leu	Gly 195	Gly	Pro	Cys	Pro	Pro 200	Ser	Ser	Asn		
					acc											(	676
Ser	_	Ile	Ser	Ala	Thr	-	Tyr	Ser	Ser	Gly	_	Arg	Met	Glu	Gly		
	205					210					215						
					agc											•	724
	Pro	Pro	Thr	Tyr	Ser	Glu	Val	Ile	Gly	His 230	Tyr	Pro	Gly	Ser			
220					225					230					235		·
					agt											-	772
Phe	Gln	His	Gln	Gln 240	Ser	Asn	Gly	Pro	Ser 245	Ser	Leu	Leu	Glu	Gly 250	Thr		
				240					245					250			
					cac											8	320
Arg	Leu	HIS	нıs 255	Ser	His	TTE	Ата	260	ьeu	GIU	Asn	ьуs	265	гÀг	GIU		
			200					200					200				
					CCC		tago	gagt	igg (	ggcc	gggg	cg co	ctgta	aggca	a .	8	371
гуѕ	GIII	270	СТУ	птэ	Pro	ьеи											
																,	270
aaad	ccgc															}	378
		210>															
		211> 212>															
				Muso	culus	5											
		4005	1.0														
		400>	1 3														
Met				Glv	Thr	Ala	Ala	Ala	Ala	Ala	Glv	Gln	Pro	Asn	Val		
1	Gly	Val	Asn	5	Thr				10		-			15			
1	Gly	Val	Asn Cys	5	Thr Cys			Ser	10		-			15			
1 Ser	Gly Cys	Val Ala	Asn Cys 20	5 Asn		Gln	Arg	Ser 25	10 Leu	Phe	Pro	Ser Val	Met 30	15 Glu	Ile		
1 Ser Thr	Gly Cys Glu	Val Ala Leu 35	Asn Cys 20 Glu	5 Asn Phe	Cys Val	Gln Gln	Arg Ile 40	Ser 25 Val	10 Leu Val	Phe Ile	Pro Val	Ser Val 45	Met 30 Val	15 Glu Met	Ile Met		
1 Ser Thr	Gly Cys Glu	Val Ala Leu 35	Asn Cys 20 Glu	5 Asn Phe	Cys	Gln Gln	Arg Ile 40	Ser 25 Val	10 Leu Val	Phe Ile	Pro Val	Ser Val 45	Met 30 Val	15 Glu Met	Ile Met		
1 Ser Thr Val	Gly Cys Glu Met 50	Val Ala Leu 35 Val	Asn Cys 20 Glu Val	5 Asn Phe Met	Cys Val Ile Ser	Gln Gln Thr 55	Arg Ile 40 Cys	Ser 25 Val Leu	10 Leu Val Leu	Phe Ile Ser Ala	Pro Val His	Ser Val 45 Tyr	Met 30 Val Lys	15 Glu Met Leu	Ile Met Ser		
1 Ser Thr Val Ala 65	Gly Cys Glu Met 50 Arg	Val Ala Leu 35 Val Ser	Asn Cys 20 Glu Val Phe	5 Asn Phe Met Ile	Cys Val Ile	Gln Gln Thr 55 Arg	Arg Ile 40 Cys His	Ser 25 Val Leu Ser	10 Leu Val Leu Gln	Phe Ile Ser Ala 75	Pro Val His 60 Arg	Ser Val 45 Tyr Arg	Met 30 Val Lys Arg	15 Glu Met Leu Asp	Ile Met Ser Asp 80		
1 Ser Thr Val Ala 65 Gly	Gly Cys Glu Met 50 Arg Leu	Val Ala Leu 35 Val Ser	Asn Cys 20 Glu Val Phe Ser	5 Asn Phe Met Ile Glu 85	Cys Val Ile Ser 70 Gly	Gln Gln Thr 55 Arg Cys	Arg Ile 40 Cys His	Ser 25 Val Leu Ser Trp	10 Leu Val Leu Gln Pro 90	Phe Ile Ser Ala 75 Ser	Pro Val His 60 Arg	Ser Val 45 Tyr Arg	Met 30 Val Lys Arg	15 Glu Met Leu Asp Val 95	Ile Met Ser Asp 80 Ser		
1 Ser Thr Val Ala 65 Gly	Gly Cys Glu Met 50 Arg Leu	Val Ala Leu 35 Val Ser	Asn Cys 20 Glu Val Phe Ser Pro	5 Asn Phe Met Ile Glu 85	Cys Val Ile Ser 70	Gln Gln Thr 55 Arg Cys	Arg Ile 40 Cys His	Ser 25 Val Leu Ser Trp	10 Leu Val Leu Gln Pro 90	Phe Ile Ser Ala 75 Ser	Pro Val His 60 Arg	Ser Val 45 Tyr Arg	Met 30 Val Lys Arg	15 Glu Met Leu Asp Val 95	Ile Met Ser Asp 80 Ser		
1 Ser Thr Val Ala 65 Gly	Gly Cys Glu Met 50 Arg Leu Gly	Val Ala Leu 35 Val Ser Ser Met Ala	Asn Cys 20 Glu Val Phe Ser Pro 100	5 Asn Phe Met Ile Glu 85 Glu	Cys Val Ile Ser 70 Gly	Gln Gln Thr 55 Arg Cys Gln	Arg Ile 40 Cys His Leu Val Ile	Ser 25 Val Leu Ser Trp Tyr 105	10 Leu Val Leu Gln Pro 90 Ala	Phe Ile Ser Ala 75 Ser Pro	Pro Val His 60 Arg Glu Pro	Ser Val 45 Tyr Arg Ser Arg	Met 30 Val Lys Arg Thr Pro 110	15 Glu Met Leu Asp Val 95 Thr	Ile Met Ser Asp 80 Ser Asp		
1 Ser Thr Val Ala 65 Gly Gly Arg	Gly Cys Glu Met 50 Arg Leu Gly Leu	Val Ala Leu 35 Val Ser Ser Met Ala 115	Asn Cys 20 Glu Val Phe Ser Pro 100 Val	5 Asn Phe Met Ile Glu 85 Glu Pro	Cys Val Ile Ser 70 Gly Pro	Gln Gln Thr 55 Arg Cys Gln Phe	Arg Ile 40 Cys His Leu Val Ile 120	Ser 25 Val Leu Ser Trp Tyr 105 Gln	10 Leu Val Leu Gln Pro 90 Ala Arg	Phe Ile Ser Ala 75 Ser Pro	Pro Val His 60 Arg Glu Pro	Ser Val 45 Tyr Arg Ser Arg Phe 125	Met 30 Val Lys Arg Thr Pro 110 Gln	15 Glu Met Leu Asp Val 95 Thr	Ile Met Ser Asp 80 Ser Asp		
1 Ser Thr Val Ala 65 Gly Gly Arg	Gly Cys Glu Met 50 Arg Leu Gly Leu	Val Ala Leu 35 Val Ser Ser Met Ala 115	Asn Cys 20 Glu Val Phe Ser Pro 100 Val	5 Asn Phe Met Ile Glu 85 Glu Pro	Cys Val Ile Ser 70 Gly Pro	Gln Gln Thr 55 Arg Cys Gln Phe	Arg Ile 40 Cys His Leu Val Ile 120	Ser 25 Val Leu Ser Trp Tyr 105 Gln	10 Leu Val Leu Gln Pro 90 Ala Arg	Phe Ile Ser Ala 75 Ser Pro	Pro Val His 60 Arg Glu Pro	Ser Val 45 Tyr Arg Ser Arg Phe 125	Met 30 Val Lys Arg Thr Pro 110 Gln	15 Glu Met Leu Asp Val 95 Thr	Ile Met Ser Asp 80 Ser Asp		
1 Ser Thr Val Ala 65 Gly Gly Arg Tyr	Gly Cys Glu Met 50 Arg Leu Gly Leu Pro 130	Val Ala Leu 35 Val Ser Ser Met Ala 115 Tyr	Asn Cys 20 Glu Val Phe Ser Pro 100 Val Leu	5 Asn Phe Met Ile Glu 85 Glu Pro	Cys Val Ile Ser 70 Gly Pro Pro His	Gln Gln Thr 55 Arg Cys Gln Phe Glu 135	Arg Ile 40 Cys His Leu Val Ile 120 Ile	Ser 25 Val Leu Ser Trp Tyr 105 Gln	10 Leu Val Leu Gln Pro 90 Ala Arg	Phe Ile Ser Ala 75 Ser Pro Ser Pro Gly	Pro Val His 60 Arg Glu Pro Arg Pro 140	Ser Val 45 Tyr Arg Ser Arg Phe 125 Thr	Met 30 Val Lys Arg Thr Pro 110 Gln	15 Glu Met Leu Asp Val 95 Thr Pro	Ile Met Ser Asp 80 Ser Asp Thr Leu Gln		
1 Ser Thr Val Ala 65 Gly Gly Arg Tyr Ser 145	Gly Cys Glu Met 50 Arg Leu Gly Leu Pro 130 Asp	Val Ala Leu 35 Val Ser Ser Met Ala 115 Tyr Gly	Asn Cys 20 Glu Val Phe Ser Pro 100 Val Leu Glu	5 Asn Phe Met Ile Glu 85 Glu Pro Gln Glu	Cys Val Ile Ser 70 Gly Pro Pro His	Gln Gln Thr 55 Arg Cys Gln Phe Glu 135 Pro	Arg Ile 40 Cys His Leu Val Ile 120 Ile Pro	Ser 25 Val Leu Ser Trp Tyr 105 Gln Ala	10 Leu Val Leu Gln Pro 90 Ala Arg Leu Gln	Phe Ile Ser Ala 75 Ser Pro Ser Pro Gly 155	Pro Val His 60 Arg Glu Pro Arg Pro 140 Pro	Ser Val 45 Tyr Arg Ser Arg Phe 125 Thr Cys	Met 30 Val Lys Arg Thr Pro 110 Gln Ile	15 Glu Met Leu Asp Val 95 Thr Pro Ser Leu	Ile Met Ser Asp 80 Ser Asp Thr Leu Gln 160		
1 Ser Thr Val Ala 65 Gly Gly Arg Tyr Ser 145 Leu	Gly Cys Glu Met 50 Arg Leu Gly Leu Pro 130 Asp Arg	Val Ala Leu 35 Val Ser Ser Met Ala 115 Tyr Gly Asp	Asn Cys 20 Glu Val Phe Ser Pro 100 Val Leu Glu Pro	5 Asn Phe Met Ile Glu 85 Glu Pro Gln Glu Glu 165	Cys Val Ile Ser 70 Gly Pro Pro His Pro 150 Gln	Gln Gln Thr 55 Arg Cys Gln Phe Glu 135 Pro Gln	Arg Ile 40 Cys His Leu Val Ile 120 Ile Pro Leu	Ser 25 Val Leu Ser Trp Tyr 105 Gln Ala Tyr	10 Leu Val Leu Gln Pro 90 Ala Arg Leu Gln Leu 170	Phe Ile Ser Ala 75 Ser Pro Ser Pro Gly 155 Asn	Pro Val His 60 Arg Glu Pro Arg Pro 140 Pro Arg	Ser Val 45 Tyr Arg Ser Arg Phe 125 Thr Cys Glu	Met 30 Val Lys Arg Thr Pro 110 Gln Ile Thr	15 Glu Met Leu Asp Val 95 Thr Pro Ser Leu Val 175	Ile Met Ser Asp 80 Ser Asp Thr Leu Gln 160 Arg		
1 Ser Thr Val Ala 65 Gly Gly Arg Tyr Ser 145 Leu	Gly Cys Glu Met 50 Arg Leu Gly Leu Pro 130 Asp Arg	Val Ala Leu 35 Val Ser Ser Met Ala 115 Tyr Gly Asp	Asn Cys 20 Glu Val Phe Ser Pro 100 Val Leu Glu Pro Asn	5 Asn Phe Met Ile Glu 85 Glu Pro Gln Glu Glu 165	Cys Val Ile Ser 70 Gly Pro Pro His	Gln Gln Thr 55 Arg Cys Gln Phe Glu 135 Pro Gln	Arg Ile 40 Cys His Leu Val Ile 120 Ile Pro Leu	Ser 25 Val Leu Ser Trp Tyr 105 Gln Ala Tyr Glu Asp	10 Leu Val Leu Gln Pro 90 Ala Arg Leu Gln Leu 170	Phe Ile Ser Ala 75 Ser Pro Ser Pro Gly 155 Asn	Pro Val His 60 Arg Glu Pro Arg Pro 140 Pro Arg	Ser Val 45 Tyr Arg Ser Arg Phe 125 Thr Cys Glu	Met 30 Val Lys Arg Thr Pro 110 Gln Ile Thr Ser Asp	15 Glu Met Leu Asp Val 95 Thr Pro Ser Leu Val 175	Ile Met Ser Asp 80 Ser Asp Thr Leu Gln 160 Arg		
1 Ser Thr Val Ala 65 Gly Gly Arg Tyr Ser 145 Leu	Gly Cys Glu Met 50 Arg Leu Gly Leu Pro 130 Asp Arg Pro	Val Ala Leu 35 Val Ser Ser Met Ala 115 Tyr Gly Asp Pro	Asn Cys 20 Glu Val Phe Ser Pro 100 Val Leu Glu Pro Asn 180	5 Asn Phe Met Ile Glu 85 Glu Pro Gln Glu 165 Arg	Cys Val Ile Ser 70 Gly Pro Pro His Pro 150 Gln	Gln Gln Thr 55 Arg Cys Gln Phe Glu 135 Pro Gln Ile	Arg Ile 40 Cys His Leu Val Ile 120 Ile Pro Leu Phe	Ser 25 Val Leu Ser Trp Tyr 105 Gln Ala Tyr Glu Asp 185	10 Leu Val Leu Gln Pro 90 Ala Arg Leu Gln Leu 170 Ser	Phe Ile Ser Ala 75 Ser Pro Ser Pro Gly 155 Asn Asp	Pro Val His 60 Arg Glu Pro Arg Pro 140 Pro Arg Leu	Ser Val 45 Tyr Arg Ser Arg Phe 125 Thr Cys Glu Ile	Met 30 Val Lys Arg Thr Pro 110 Gln Ile Thr Ser Asp 190	15 Glu Met Leu Asp Val 95 Thr Pro Ser Leu Val 175 Ser	Ile Met Ser Asp 80 Ser Asp Thr Leu Gln 160 Arg		
1 Ser Thr Val Ala 65 Gly Gly Arg Tyr Ser 145 Leu Ala Met	Gly Cys Glu Met 50 Arg Leu Gly Leu Pro 130 Asp Arg Pro Leu	Val Ala Leu 35 Val Ser Ser Met Ala 115 Tyr Gly Asp Pro Gly 195	Asn Cys 20 Glu Val Phe Ser Pro 100 Val Leu Glu Pro Asn 180 Gly	5 Asn Phe Met Ile Glu 85 Glu Pro Gln Glu 165 Arg	Cys Val Ile Ser 70 Gly Pro His Pro 150 Gln Thr Cys	Gln Gln Thr 55 Arg Cys Gln Phe Glu 135 Pro Gln Ile Pro	Arg Ile 40 Cys His Leu Val Ile 120 Ile Pro Leu Phe Pro 200	Ser 25 Val Leu Ser Trp Tyr 105 Gln Ala Tyr Glu Asp 185 Ser	10 Leu Val Leu Gln Pro 90 Ala Arg Leu Gln Leu 170 Ser Ser	Phe Ile Ser Ala 75 Ser Pro Ser Pro Gly 155 Asn Asp Asn	Pro Val His 60 Arg Glu Pro Arg Pro 140 Pro Arg Leu Ser	Ser Val 45 Tyr Arg Ser Arg Phe 125 Thr Cys Glu Ile Gly 205	Met 30 Val Lys Arg Thr Pro 110 Gln Ile Thr Ser Asp 190 Ile	15 Glu Met Leu Asp Val 95 Thr Pro Ser Leu Val 175 Ser Ser	Ile Met Ser Asp 80 Ser Asp Thr Leu Gln 160 Arg Thr		
1 Ser Thr Val Ala 65 Gly Gly Arg Tyr Ser 145 Leu Ala Met	Gly Cys Glu Met 50 Arg Leu Gly Leu Pro 130 Asp Arg Pro Leu Cys	Val Ala Leu 35 Val Ser Ser Met Ala 115 Tyr Gly Asp Pro Gly 195	Asn Cys 20 Glu Val Phe Ser Pro 100 Val Leu Glu Pro Asn 180 Gly	5 Asn Phe Met Ile Glu 85 Glu Pro Gln Glu 165 Arg	Cys Val Ile Ser 70 Gly Pro His Pro 150 Gln Thr	Gln Gln Thr 55 Arg Cys Gln Phe Glu 135 Pro Gln Ile Pro Gly	Arg Ile 40 Cys His Leu Val Ile 120 Ile Pro Leu Phe Pro 200	Ser 25 Val Leu Ser Trp Tyr 105 Gln Ala Tyr Glu Asp 185 Ser	10 Leu Val Leu Gln Pro 90 Ala Arg Leu Gln Leu 170 Ser Ser	Phe Ile Ser Ala 75 Ser Pro Ser Pro Gly 155 Asn Asp Asn	Pro Val His 60 Arg Glu Pro Arg Pro 140 Pro Arg Leu Ser Pro	Ser Val 45 Tyr Arg Ser Arg Phe 125 Thr Cys Glu Ile Gly 205	Met 30 Val Lys Arg Thr Pro 110 Gln Ile Thr Ser Asp 190 Ile	15 Glu Met Leu Asp Val 95 Thr Pro Ser Leu Val 175 Ser Ser	Ile Met Ser Asp 80 Ser Asp Thr Leu Gln 160 Arg Thr		
1 Ser Thr Val Ala 65 Gly Gly Arg Tyr Ser 145 Leu Ala Met	Gly Cys Glu Met 50 Arg Leu Gly Leu Pro 130 Asp Arg Pro Leu Cys 210	Val Ala Leu 35 Val Ser Ser Met Ala 115 Tyr Gly Asp Pro Gly 195 Tyr	Asn Cys 20 Glu Val Phe Ser Pro 100 Val Leu Glu Pro Asn 180 Gly Ser	5 Asn Phe Met Ile Glu 85 Glu Pro Gln Glu 165 Arg Pro Ser	Cys Val Ile Ser 70 Gly Pro His Pro 150 Gln Thr Cys	Gln Gln Thr 55 Arg Cys Gln Phe Glu 135 Pro Gln Ile Pro Gly 215	Arg Ile 40 Cys His Leu Val Ile 120 Ile Pro Leu Phe Pro 200 Arg	Ser 25 Val Leu Ser Trp Tyr 105 Gln Ala Tyr Glu Asp 185 Ser Met	10 Leu Val Leu Gln Pro 90 Ala Arg Leu Gln Leu 170 Ser Ser Glu	Phe Ile Ser Ala 75 Ser Pro Ser Pro Gly 155 Asn Asp Asn Gly	Pro Val His 60 Arg Glu Pro Arg Pro 140 Pro Arg Leu Ser Pro 220	Ser Val 45 Tyr Arg Ser Arg Phe 125 Thr Cys Glu Ile Gly 205 Pro	Met 30 Val Lys Arg Thr Pro 110 Gln Ile Thr Ser Asp 190 Ile Pro	15 Glu Met Leu Asp Val 95 Thr Pro Ser Leu Val 175 Ser Ser Thr	Ile Met Ser Asp 80 Ser Asp Thr Leu Gln 160 Arg Thr Ala		



## -15-

```
Ser Asn Gly Pro Ser Ser Leu Leu Glu Gly Thr Arg Leu His His Ser
                245
                                     250
His Ile Ala Pro Leu Glu Asn Lys Glu Lys Glu Lys Gln Lys Gly His
            260
                                 265
                                                     270
Pro Leu
      <210> 14
      <211> 693
      <212> DNA
      <213> Homo Sapiens
      <220>
      <221> unsure
      <222> (639)...(639)
      <223> a, c, g, or t/u
      <400> 14
tttttttgca agctctctta gcttgtgcat tcagaccaga catcacatgt aaatatttat
                                                                        60
acacagggag gtgggagggg agggccacac gatgcgttgc tgcgcccccc gccttcctct
                                                                       120
cactectett ctaagaageg eggagtgtte tgeettttea eetaegeage eecageeegg
                                                                       180
ccccctggg gaccctagag agggtgtcct ttctgtttat ccttctcttt gctccagatg
                                                                       240
gctgcgctct ctaggggcgc gatgtgtgtg tgggggaacc cggtccccct ccagcaagga
                                                                       300
gggcggccca ctgctctgct ggtgctggaa ggaggacccc gggtagtggc cgatgacctc
                                                                       360
qctqtaqqtq qqcqqcgcc cctccatgcg cccgccgctg ccgtagcacg tggcgctgat
                                                                       420
gcccgagtta ctgctggggg ggcaggggcc gcccagcctg gcactatcca tcaggtcact
                                                                       480
gtcgaagatg gttctgtttg ggggtgcgcg caccgactcc cggttcagtt ccagctgctg
                                                                       540
cteggggtee egaagetgga gggtgeaggg geeetggtag ggtggggete etecegtetg
                                                                       600
acagegagat ggtgggegge agtegatete gtgetgeang taeggatagg tgggetggaa
                                                                       660
gcggtggaag cgctcccgct gggcgaaagg cgg
                                                                       693
      <210> 15
      <211> 475
      <212> DNA
      <213> Mus Musculus
      <400> 15
aattcqtcqa catqqcttqa tqqqqqtcaa cqqcaccqcc qccqccqccq ccqqqcaqcc
                                                                        60
caatqtetee tgegegtgea actgeeageg etetttgtte eecageatgg agateaegga
                                                                       120
gctggagttc gtgcaaatcg tggtcatcgt ggtagtgatg atggtgatgg tggttatgat
                                                                       180
tacgtgcctg ctgagccact acaagctgtc agcccgctcc ttcatcagcc gacacagcca
                                                                       240
ggccaggagg agagacgatg gactgtcctc ggaaggatgc ctctggccct cagagagtac
                                                                       300
ggtgtcaggt ggaatgccgg agccacaggt ctatgccccg cctcggccca ctgaccgact
                                                                       360
cgctgtgccc cccttcatcc agcggagccg attccaaccc acctacccct acctgcagca
                                                                       420
cqaaattqcc ctqccaccca ccatctcact qtctqatqqq qaqqaqccc caccc
                                                                       475
      <210> 16
      <211> 8093
      <212> DNA
      <213> Homo Sapiens
      <220>
      <221> unsure
      <222> (6477)...(6477)
      <223> c or t/u
```

<222> (6837)...(6837)

<223> a or c

<221> unsure

<400> 16



			-10-			
ctcagctccc	tgtggtgggg	gatggcagag	gcttcccgct	ccccgcagct	ggtttgcaca	60
gcctcccgac	tgtgccgtgg	tgtctccttc	cctaaagtgg	gacagtcgtt	tctgtgtcct	120
gctggcctct	gaggaacaga	cgtgtgtgag	aggccttcag	ggcctgatgg	ctggggtggt	180
gacagtgcct	ggagaatggg	tggggactgg	aggggccagg	tggctaacca	ctctcctctt	240
ccatggcagc	ggagctggag	ttcgcccaaa	tcatcatcat	cgtcgtggtg	gtcacggtga	300
tggtggtggt	catcgtctgc	ctgctgaacc	actacaaagt	ctccacgcgg	tccttcatca	360
		aggcgggagg				420
		cggctgggcg				. 480
		tccttcatcc				540
		gagattgatc				600
		gggccctgca				660
		gtgagggccc				720
		agcgggggtc				780
gtgcaagcac	ctgcagcagt	aacgggagga	tggaggggcc	acccccaca	tacagcgagg	840
		gcctctttcc				900
		cagaacaatg				960
		ctggtctgat				1020
		ccgctgggcc				1080
		caaatgagca				1140
		actgaaatga				1200
		ggttgggatg				1260
		aaataaaacc				1320
		tgaggccaga				1380
		tattgtgggg				1440
		tttaaaaata				1500
		atgagtgcaa				1560
		tgttgaaaat				1620
		tgtggattgt				1680
		agatatttgg				1740
		tgttgcagga				1800
		ggaagataag				1860
		tgctactctt				1920
		tcatgcagtg				1980
		cactatagca				2040
		tgcaaggtgg				2100
		ctctcccct				2160
		ctcccagcag				2220
cgtgtgggag	tggtgtgggt	ggtggttttc	ttatgctttg	gaagccccta	gaaataatga	2280
		gatcgtggta				2340
		aaaggaatgc				2400
ggattttacc	aaacccttcc	ccaggccagt	tttgtactga	aggcaagaac	tggacagtca	2460
		gtgactgaag				2520
aaaatgcaaa	ctagaaaact	aattttaaat	attgttagtt	ttaatatttc	ctgatattta	2580
caaatattca	ttcttatata	caatgaaaaa	aataactttc	ttctgcagat	gtaagcactg	2640
gcttttataa	gagcagcagc	caacacgttt	agcagacact	gcgcgtggag	aagggcttat	2700
ctgcagtaca	ctctgccatg	tggagggtgg	gcctctgtgg	cctcttcaca	taacaagatg	2760
agctggaatg	atgattccat	gactcccacc	tatgcagcct	taaagccaaa	tccgcgtgtg	2820
tgtgtttgtg	tctgtctgtg	ggtctcgaag	gtgatccgtc	ggtgcggtgg	ctctgtgctg	2880
taactggaga	gactgttcca	aaccccaaga	gttgtctgat	cctagtctgt	tcccttctgc	2940
ttcttacctc	tgtagatagg	tcactggttt	ttgtttgttt	gttttgagga	ttggaatttc	3000
cattacattc	atcctttgca	cacagtaaca	tccacagaac	tagtccaact	cttaaaagga	3060
gagaggaaaa	acacaggcac	cagttgtcag	ctcatgctta	caacctgtgt	ggaagtatat	3120
acagttgaga	gtcacagtgg	aggttctgag	actggattca	gtcttgttcc	agtgacagtt	3180
ggaaggcctc	tgctggagag	acaccagctc	tcagggcaga	gattggcttg	gggccagaag	3240
gaccctcccc	aaccctggag	acaccctgaa	ggttcactgg	ctctccagat	tagcctctct	3300
		aggagcccgt				3360
		tgtgcccaca				3420
		tttggtgaag				3480
		cttctctacc				3540
		tgagtatatg				3600
agataattac	ataattcaga	tacctttaat	catctttcaa	gaaagaggct	cctcccattc	3660



			-1/-			
aaccacccta	gagaactgcc	tttgttaaat	agttatttaa	agactcatac	atatcaaacc	3720
atgactttga	aaggtcttcg	aggctggggc	tctgtaatga	attagtttaa	aagccaaggt	3780
cataacatga	attgatggtc	aatttccctt	cagcagaagg	aaaaggtgat	ttagatcagt	3840
agctcttttg	aaggttgtgg	ctgacctgtt	cataccgtgt	cgcctcatgg	ctagtgtggc	3900
		gaagatacaa				3960
		agaacccatg				4020
		cttagattat				4080
		acactcctgg				4140
		tcttgaatcc				4200
		tagcattctc			_	4260
		tatgtatttc				4320
		caagcatgtc				4380
		aatcccaaga				4440
		cactaatttt				4500
		cctcctgaca				4560
		tctccgtttg				4620
						4620
		gaagcacttt				
		tctgaaccaa				4740
		cttcctttta				4800
		attgctagta				4860
		tggcgttggt				4920
		ccatgcagcc				4980
		gaattttgct				5040
		tccaaagctc				5100
		tttgtgttgc				5160
		acatgctcca				5220
		tggcctactg				5280
		cttggtgcga				5340
		agttctcagc				5400
		cgctacagat				5460
		tacatttttt				5520
		cagagttcaa				5580
		tgctgctgct				5640
		gctaagaaag				5700
		tgtgtaatgc				5760
		atatatatgt				5820
	<del>-</del>	aaggtgcctc				5880
		gatgctccca				5940
		tcttatgttt				6000
		cccaatgggt				6060
atgtatagat	gataccaatt	ttaacagaaa	tggcatagaa	tttgtgaatg	cctatgtgct	6120
-		atttgcaaat				6180
		atattataac				6240
		atatagcaat				6300
		aaaatcccac				6360
		ctcagctgga				6420
tgttgttttt	caacttgctt	tataatctcc	tgcatctatc	tcctgctgta	gcatcaygaa	6480
		agtgcacatt				6540
taagtaaatc	agcctgcagc	agaagacttt	gttcagctcc	agaggcatct	gtgaccgtct	6600
		ctttttcttt				6660
		aagaatacct				6720
cctgttctta	gaaaatgtgt	ttagttatgg	gttagcacta	gaagagactt	ggctgtcagc	6780
cagccaagtg	aaggacctct	catccattcc	cattcatgtc	ccatcataat	acggacmcaa	6840
aaagcaaact	cggttttgcc	atcagttaga	aattacgttt	tggattgtat	attgttacat	6900
ctctcttcca	gcttagtttt	tagtgtctga	ttgtgacctc	tgcatttatc	ttcaaatacc	6960
		caagaaaagt				7020
		cctttcgagt				7080
		cagcttattc				7140
		gtgtatgttc				7200
		caaatgacag				7260
		ggattaaaaa				7320
-	•	-	- <del>-</del>	-		



-18-

gccgtaaaaa	gttgacactt	ttgttgttgt	ggatcctgcg	tgtctagacc	cacgtgttgt	7380
ttccatcgta	tactgtaggg	tgcacccctt	gggattcatc	attaagaact	gaggctcact	7440
gttgtcagaa	acaaagctcc	caccccccag	gttcaacctt	gtgggagaac	tgttgagcat	7500
gagaatgttc	tagactcaga	ggtactaaaa	tttgttacca	catcattgct	tcctttctac	7560
	gaggcttaaa					7620
tggtatgttg	ctatttttca	tttcatagct	ttcaaaaatc	atgctaattg	tatacttgtc	7680
tagtttaagg	ctattttaaa	atatgtacaa	tactattcac	agcatttagt	tcgtttaatt	7740
tttattataa	agcaatctac	taaaaaagta	caactgtatt	tgaacttttc	aatagttgtt	7800
tgtgagctat	gataatcaaa	agtcattaaa	gtcttttta	acaaacattc	gtgcttactt	7860
ttcaacataa	ttcccagtta	tatacagaaa	aagatttcca	cctgtcacgt	atctgcctct	7920
tttacctgag	caatggtgta	gttcttagac	ctaaggtctg	taattgcaat	acttttaaag	7980
aaagatgttg	ctctaagtgc	tgtttgttag	ttatgaaatc	agatttttct	gcttgttctt	8040
aatgctgtgg	tcaaaccata	gcacaaaatc	attaaaaata	atcagcggca	tac	8093

```
<210> 17
<211> 513
<212> DNA
<213> Homo Sapiens
<220>
<221> unsure
<222> (8)...(9)
<223> a, c, g, or t/u
<221> unsure
<222> (28)...(28)
<223> a, c, g, or t/u
<221> unsure
<222> (34)...(34)
\langle 223 \rangle a, c, g, or t/u
<221> unsure
<222> (42)...(42)
<223> a, c, g, or t/u
<221> unsure
<222> (44)...(44)
<223> a, c, g, or t/u
<221> unsure
<222> (46)...(46)
<223> a, c, g, or t/u
<221> unsure
<222> (49)...(49)
<223> a, c, g, or t/u
<221> unsure
<222> (53)...(53)
<223> a, c, g, or t/u
<221> unsure
<222> (55)...(55)
\langle 223 \rangle a, c, g, or t/u
<221> unsure
<222> (66)...(66)
<223> a, c, g, or t/u
```





<221> unsure <222> (410)...(410) <223> a, c, g, or t/u

## <400> 17

aggggganna	gagctgatcc	ttgtatanct	gacnactttg	cnananacnc	aanangaaga	60
ggaagnagcg	ccggtgcaca	cacaccagag	cgtttcgccc	atttgaacct	ttacctcctt	120
agcgagatgc	tgaatcgctg	atttatggca	tatcatccgc	cttgggcact	tttctcgact	180
atcctgttat	tcacctgtga	actgggacat	caataatgat	gggctcacta	gatcaaggga	240
gagaaagact	gcatacaaat	aaatgcgtaa	aagcactgat	taacctatga	cacgtgctgg	300
atagggaatc	aacacatgac	aaggttcacg	gtatacgccc	ttcatatgct	ggtctacata	360
ggtctgcagg	cgactctgga	cctgaacgag	tatcatagcg	agccgagcan	cctagcctgc	420
	acgtgtagct					480
	gctgtggacg					513